

# **MANDATOS DE ACCESO ABIERTO A PUBLICACIONES EN H2020 Y PLAN ESTATAL 2017-2020 Y SERVICIOS DE DIGITAL.CSIC**

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DIGITAL.CSIC, URICI

20 de abril, 2018

# Vías del Acceso Abierto



repositorios

- Institucionales (p.e, DIGITAL.CSIC)
- Temáticos (p.e EuropePMC, arXiv)
- Internacionales (p.e Zenodo)

revistas

- Revistas de acceso abierto de “nuevos” editores (p.e todas las de PLOS, MDPI, Frontiers, Copernicus..) o de editores “tradicionales” (p.e, Nature Communications de Nature Research, New Journal of Physics de IoP..)
- Revistas de suscripción con opción para publicar en acceso abierto (casi todas las de grandes grupos editoriales)

# Mandato de acceso abierto a publicaciones en H2020



## SELF-ARCHIVING 'GREEN' OPEN ACCESS

deposit the final peer-reviewed manuscript in a repository of your choice.

*Researchers must ensure open access to the publication within at most 6 months (12 months for publications in the social sciences and humanities).*



## OPEN ACCESS PUBLISHING 'GOLD' OPEN ACCESS

publish in open access journals or in hybrid journals.

*Article processing charges are eligible for reimbursement during the duration of your project. Hybrid journals sell subscriptions (i.e. closed access) AND offer the option of making some individual articles open access.*



## BOTH OPTIONS ARE POSSIBLE

If the gold route is chosen the article must also be deposited in a repository to comply with Article 29.2.

**Qué acceso abierto:** como mínimo, leer, imprimir y descargar gratuitamente

**Qué tipo de resultados:** artículos de revistas peer-reviewed.

Acceso abierto *recomendado* para libros, monografías, comunicaciones a congresos, literatura gris

**Qué proyectos:** los financiados o co-financiados por alguna convocatoria H2020 (incluidos proyectos Euratom)

**Qué versión:** versión editorial o de autor revisada (“postprint”, “accepted author manuscript”)

### **Qué embargos:**

6 meses (12 Humanidades) tras la publicación online para acceso abierto a través de repositorios.

Acceso abierto inmediato a través de revistas

**Qué metadatos en repositorios:** agencia financiadora, nombre del proyecto, acrónimo, número de proyecto, fecha de publicación online, periodo de embargo, identificador persistente

**Qué licencias:** la *recomendación* es conservar el copyright y elegir licencias para publicación.

Licencias Creative Commons (CC), CC-BY en particular, *recomendadas* para publicaciones en acceso abierto

**Qué financiación para APCs:** durante los proyectos. No límites estipulados sobre número de artículos para publicar o máximos en APCs y deben ser incluidas en el presupuesto

# Matrices en mandato ERC (publicaciones)



Acceso abierto a todas las publicaciones científicas revisadas por pares (artículos, comunicaciones, libros, monografías) de proyectos Frontiers Research, Proof of Concept, CSA

Embargos mayores de los marcados por el mandato (6/12 meses) , aceptables para publicaciones resultantes después del proyecto



Repositorios temáticos recomendados: arXiv (Físicas, Ingenierías) y EuropePMC (Biomedicina), OAPEN (para libros, monografías)

Repositorios institucionales

Repositorios centralizados (ZENODO)



BPCs (Book Processing Charges) pueden ser cubiertos para publicaciones durante los proyectos

# Mandato de acceso abierto a publicaciones en Planes Estatales



## Plan Estatal 2013-2016

**Acceso abierto a PDF editorial/postprint de artículo de revista en un repositorio en un plazo no superior a 6 meses (12 en Humanidades) tras publicación oficial o**

**Acceso abierto inmediato a través de publicación en acceso abierto (APCs como gastos de publicación del proyecto)**

## Plan Estatal 2017-2020

**Acceso abierto a PDF editorial/postprint de artículo de revista en un repositorio en un plazo no superior a 6 meses (12 en Humanidades) tras publicación oficial**

**Los proyectos *podrán* incluir un plan de gestión de datos**

**Acceso abierto de datos de investigación a través de un repositorio tras la finalización del proyecto**

**Acceso abierto como criterio de evaluación de investigadores y de actividades financiadas**

# Ejemplo de convocatoria de MINECO



MINISTERIO  
DE ECONOMÍA, INDUSTRIA  
Y COMPETITIVIDAD



Resolución de la Presidencia de la Agencia Estatal de Investigación, por la que se aprueba la convocatoria del año 2017, de tramitación anticipada, para la concesión de las acreditaciones y ayudas públicas de «Centros de Excelencia Severo Ochoa» y de «Unidades de Excelencia María de Maeztu» del Programa Estatal de Fomento de la Investigación Científica y Técnica de Excelencia, Subprograma Estatal de Fortalecimiento Institucional, en el marco del Plan Estatal de Investigación Científica y Técnica y de Innovación 2013-2016.

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### Preámbulo

### Capítulo I. Disposiciones generales

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Artículo 2. *Finalidad.*

Artículo 3. *Régimen de concesión y normativa aplicable.*

Artículo 4. *Definiciones.*

### Capítulo II. Requisitos generales de los beneficiarios

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Artículo 6. *Obligaciones de los beneficiarios y publicidad de las ayudas concedidas.*

Artículo 7. *Requisitos de los «Centros de Excelencia Severo Ochoa» y de las «Unidades de Excelencia María de Maeztu».*

### Capítulo III. Características de la actividad subvencionada

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Artículo 9. *Gastos subvencionables.*

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### Capítulo IV. Régimen económico de las ayudas

Artículo 11. *Financiación de las ayudas.*

Artículo 12. *Incompatibilidades.*

### Capítulo V. Reglas del procedimiento de concesión

Artículo 13. *Órganos competentes para instruir y resolver el procedimiento de concesión.*

Artículo 14. *Comunicaciones entre la Administración y los interesados.*

Artículo 15. *Plazo y forma de presentación de solicitudes.*

- **Artículo 6. Obligaciones y responsabilidades de los beneficiarios**

**2. Cuando los resultados no sean susceptibles de protección de derechos de propiedad industrial o intelectual, las publicaciones científicas resultantes de la financiación otorgada al amparo de la presente convocatoria deberán estar disponibles en acceso abierto, de acuerdo con el artículo 37 de la Ley 14/2011, de 1 de junio.**

**A tales efectos, los autores podrán, con la mayor brevedad posible, optar por publicar en revistas de acceso abierto o bien por autoarchivar en repositorios institucionales o temáticos de acceso abierto, recogidos en la plataforma Recolecta de la Fundación Española para la Ciencia y la Tecnología (FECYT) u otros repositorios promovidos por las propias instituciones, los trabajos científicos que hayan sido aceptados para su publicación en publicaciones seriadas o periódicas.**

**La publicación se producirá en un plazo no superior a los seis meses tras su publicación comercial, salvo en el área de Humanidades y Ciencias Sociales, donde el plazo establecido no será superior a un año.**



*“No quiero gastarme dinero del proyecto en pagar APCs de acceso abierto”:* Solo te queda, entonces, la vía de repositorios para garantizar acceso abierto a tus resultados (y hay que ver los periodos de embargo de la revista sobre PDF editorial/postprint)

Elsevier:  
embargos de 0 a 36 meses

Oxford University Press:  
embargos de 0 a 24 meses

Wiley y Springer:  
embargos de 12 meses

American Chemical Society:  
embargos de 12 meses

IEEE: 0 embargo

Taylor&Francis:  
embargos de 0 a 18 meses

Cambridge University Press:  
embargos de 6 meses



# Ejemplo de política editorial para repositorios

## Para las revistas Nature Research de suscripción

- ***Nature Research's policies are compatible with the vast majority of funders' open access and self-archiving mandates.*** (...) When a research paper is accepted for publication in an Nature Research journal, **authors are encouraged** to submit the Author's Accepted Manuscript to PubMedCentral or other appropriate funding body's archive, for public release six months after first publication. In addition, authors are encouraged **to archive this version of the manuscript in their institution's repositories** and, if they wish, on their personal websites, **also six months after the original publication.**
- <https://www.nature.com/authors/policies/license.html>

# **CUMPLIMIENTO A TRAVÉS DE DIGITAL.CSIC Y ALGUNOS CONSEJOS**

# Recuerda....

- **Empezar a pensar en el cumplimiento del mandato en la fase de escritura del proyecto. Esto implica:**

1. Estimar el número de artículos de revistas resultados del proyecto
2. Comprobar las políticas editoriales para repositorios de las revistas preferentes
3. Estimar las APCs si se decide publicar en acceso abierto (sin llegar a presupuestos desorbitantes)
4. Todo el consorcio del proyecto, y no solo el equipo CSIC, debe consensuar su estrategia de acceso abierto

- **Una vez aprobado el proyecto tener en cuenta:**

1. El mandato afecta a cualquier artículo de revista resultado del proyecto, por pequeña que haya sido la contribución económica del proyecto H2020/MINECO y aunque el CSIC no sea el coordinador del proyecto
2. Incluir en los *acknowledgements* del artículo la referencia y acrónimo/nombre del proyecto
3. En DIGITAL.CSIC deben depositarse los resultados de los participantes CSIC en el proyecto
4. El depósito en DIGITAL.CSIC no impide la difusión de esos resultados a través de otros repositorios/webs

- **NO se está cumpliendo con el mandato H2020 si se deposita:**

1. Un preprint (versión no revisada de autor)
2. Un postprint o un PDF editorial con un embargo superior a 6 meses (12 meses en Humanidades)
3. Usar como “*repositorio*” la web del proyecto, sitios sociales académicos como Research Gate, Academia.edu, Dropbox

- **La Comisión Europea hace seguimiento del grado de cumplimiento de manera regular (y hay consecuencias)**

- **El mandato de MINECO SÍ acepta el acceso abierto embargado**

# PASOS PARA CUMPLIR LOS MANDATOS H2020/MINECO A TRAVÉS DE DIGITAL.CSIC

3

Indexación por:



*Recolecta*  
RECOLECTOR DE CIENCIA ABIERTA



## Carga del artículo en DIGITAL.CSIC:

- A través del Servicio de Archivo Delegado (Oficina Técnica del repositorio o tu biblioteca)
- Descripción y etiquetado del artículo según los requisitos de H2020/MINECO
- Generación de un identificador único y persistente (handle)

1

## Publicación de los resultados del proyecto en una revista con revisión de pares:

Permisos editoriales para su difusión en acceso abierto en el repositorio

APCs para la publicación en acceso abierto

# ¿Cómo puedo depositar los resultados de mi proyecto H2020/MINECO en DIGITAL.CSIC?

Aprovecha los servicios del personal bibliotecario CSIC



# ¿Qué es OpenAire?



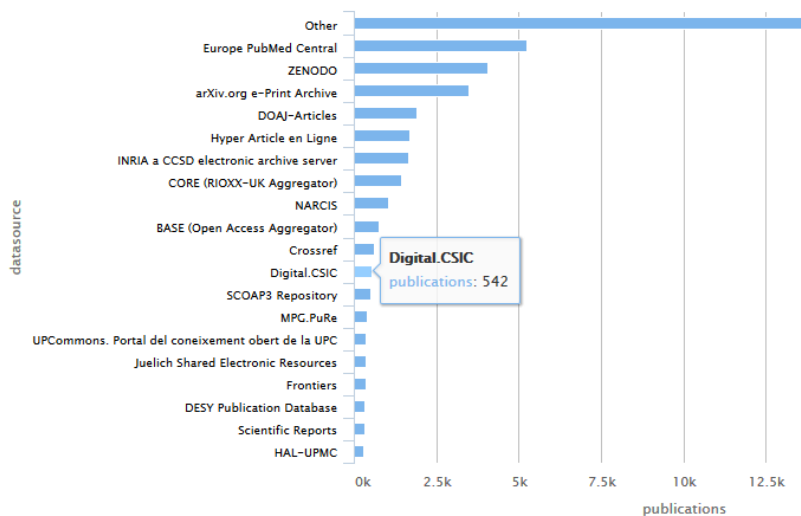
PARTICIPATE

## ABOUT DATA PROVIDERS

### TOP 20 DATA PROVIDERS FOR H2020 PUBLICATIONS



H2020 Publications by datasource (top 20)



[Resultados de proyectos CSIC H2020 en DIGITAL.CSIC](#)



PARTICIPATE SEARCH

## TB-ACCELERATE

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### APP BOX

Title	Integrating genomics, epidemiology and evolution to accelerate tuberculosis eradication
Funding	EC   H2020   ERC   ERC-STG
Call	ERC-2014-STG
Contract (GA) number	638553
Start Date	2015/07/01
End Date	2020/06/30
Open Access mandate	yes
Data Pilot	no
Organizations	CSIC, FISABIO
More information	<a href="#">Detailed project information (CORDIS)</a>

Publications (12) Research Data (0) Statistics

[view all 12](#)

A novel strategy based on genomics and specific PCR reveals how a multidrug-resistant *Mycobacterium tuberculosis* strain became prevalent in Equatorial Guinea 15 years after its emergence  
Pérez-Lago, Laura; Herranz, Marta; Comas, Iñaki; Sierra, Olalla; Bouza, Emilio; García de Viedma, Darío (2016)  
Projects: [EC | TB-ACCELERATE \(638553\)](#)

1. [Agregador de ciencia europea y otras regiones en acceso abierto financiado por la Comisión Europea](#)

2. Gestor de proyectos EC

3. Portal de resultados de proyectos EC y de algunas agencias nacionales

# CASO 1: Publicación en revista de acceso abierto y subida del PDF editorial en DIGITAL.CSIC

## 2. Publicación de resultados en acceso abierto

## 3. Depósito y marcado en DIGITAL.CSIC

**CORDIS**  
Community Research and Development Information Service

European Commission > CORDIS > Projects and Results > Integrating genomics, epidemiology and evolution to accelerate tuberculosis eradication

NEWS & EVENTS PROJECTS & RESULTS RESEARCH\*EU MAGAZINES

**TB-ACCELERATE**  
Project ID: 638553  
Funded under: H2020-EU.1.1 - EXCELLENT SCIENCE - European Research Council (ERC)

**Integrating genomics, epidemiology and evolution to accelerate tuberculosis eradication**

From 2015-07-01 to 2020-06-30, ongoing project

**Project details**

Total cost:	Topic(s):
EUR 1 671 875	ERC-SG-2014 - ERC Starting Grant
EU contribution:	Call for proposal:
EUR 1 671 875	ERC-2014-STG See other projects for this call
Coordinated in:	Funding scheme:
Spain	ERC-STG - Starting Grant

**Objective**

When the scale of the tuberculosis (TB) epidemic was highlighted by its declaration as a "Global Emergency" by WHO in 1993, it was envisaged that the efficient use of existing tools would result in a progressive decline towards eradication. This has not occurred. At the current pace of decline in TB incidence the Millennium objective to eradicate it by 2050 will not be met. Predictions of epidemiological models were inaccurate and current control programs and technologies ha...

**Host Institution**

AGENCIA ESTATAL CONSEJO SUPERIOR DE INVESTIGACIONES CIENTÍFICAS Spain

## 1. Aprobación de la propuesta

**SCIENTIFIC REPORTS**

OPEN

### Gene expression models based on a reference laboratory strain are poor predictors of *Mycobacterium tuberculosis* complex transcriptional diversity

Álvaro Chiner-Oms<sup>1</sup>, Fernando González-Candelas<sup>1,2</sup> & Iñaki Comas<sup>1,3</sup>

Received: 22 November 2017  
Accepted: 19 February 2018  
Published online: 28 February 2018

Every year, species of the *Mycobacterium tuberculosis* complex (MTBC) kill more people than any other infectious disease caused by a single agent. As a consequence of its global distribution and parallel evolution with the human host the bacteria is not genetically homogeneous. The observed genetic heterogeneity has relevance at different phenotypic levels, from gene expression to epidemiological dynamics. However, current systems biology datasets have focused on the laboratory reference strain H37Rv. By using large expression datasets testing the role of almost two hundred transcription factors, we have constructed computational models to grab the expression dynamics of *Mycobacterium tuberculosis* H37Rv genes. However, we have found that many of those transcription factors are deleted or likely dysfunctional across strains of the MTBC. As a result, we failed to predict expression changes in strains with a different genetic background when compared with experimental data. These results highlight the importance of designing systems biology approaches that take into account the genetic diversity of *tubercle bacilli*, or any other pathogen, if we want to identify universal targets for vaccines, diagnostics and treatments.

Tuberculosis has been a scourge to humankind for millennia<sup>1</sup>. Today, TB is the leading cause of death by a single infectious agent worldwide<sup>2</sup>. In humans, the disease is caused by *Mycobacterium tuberculosis* and *Mycobacterium africanum*, which belong to the *Mycobacterium tuberculosis* complex (MTBC), along with other species that cause the disease in animals. The bacterium infects the host through the respiratory tract. Once in the lungs, it is phagocytized by macrophages, which typically are encapsulated in a granuloma<sup>3</sup>. The bacteria can be dormant and survive inside the granuloma during months, years, or even decades in a so-called latent disease state called latency<sup>4</sup>. The transition from latency to an active disease state depends on biological features of the bacteria, the host, environmental factors and the interactions among all of them<sup>5</sup>. These interactions are not completely understood yet<sup>6</sup>. Moreover, animal models are widely used but they do not reproduce perfectly the human-pathogen interaction<sup>7</sup>. One way to approach the complexity of the host-pathogen-environment triangle is through systems biology. In the case of TB, systems biology approaches have produced encouraging results in the identification of persistence genes<sup>8</sup>, the pharmacokinetics and pharmacodynamics of TB drugs inside the granuloma<sup>9,10</sup>, and the identification of drug resistance mechanisms<sup>11</sup>. Overexpression experiments and chromatin-immune-precipitation sequencing (ChIP-Seq) data have been used to produce a detailed map of the interactions and regulatory logic of more than 200 transcription factors (TFs) in H37Rv, the laboratory reference strain<sup>12,13</sup>. The enormous amount of data generated is publicly available and can be used to study the regulatory interactions of the bacteria in several ways<sup>14</sup>.

However, little attention has been paid to the fact that H37Rv is a clinical strain used in laboratories for dec-

DIGITAL.CSIC / Biología y Biomedicina / Instituto de Biomedicina de Valencia (IBV) / (IBV) Artículos

English español

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Estadísticas Visualizar otros formatos: MARC | Dublin Core | RDF | ORE | MODS | METS | DIDL

Compartir tu historia de Acceso Abierto

**Título:** Gene expression models based on a reference laboratory strain are poor predictors of *Mycobacterium tuberculosis* complex transcriptional diversity

**Autor:** Chiner-Oms, Álvaro; González-Candelas, Fernando; Comas, Iñaki

**Fecha de publicación:** 28-feb-2018

**Editor:** Nature Publishing Group

**Citación:** Scientific Reports 8(1):3813 (2018)

**Resumen:** Every year, species of the *Mycobacterium tuberculosis* complex (MTBC) kill more people than any other infectious disease caused by a single agent. As a consequence of its global distribution and parallel evolution with the human host the bacteria is not genetically homogeneous. The observed genetic heterogeneity has relevance at different phenotypic levels, from gene expression to epidemiological dynamics. However, current systems biology datasets have focused on the laboratory reference strain H37Rv. By using large expression datasets testing the role of almost two hundred transcription factors, we have constructed computational models to grab the expression dynamics of *Mycobacterium tuberculosis* H37Rv genes. However, we have found that many of those transcription factors are deleted or likely dysfunctional across strains of the MTBC. As a result, we failed to predict expression changes in strains with a different genetic background when compared with experimental data. These results highlight the importance of designing systems biology approaches that take into account the genetic diversity of *tubercle bacilli*, or any other pathogen, if we want to identify universal targets for vaccines, diagnostics and treatments.

**Descripción:** 13 Páginas, 7 figuras. Contiene información suplementaria en: 10.1038/s41598-018-22237-5

**Versión del editor:** <http://dx.doi.org/10.1038/s41598-018-22237-5>

**URI:** <http://hdl.handle.net/10261/161882>

**OpenAIRE**

Gene expression models based on a reference laboratory strain are poor predictors of *Mycobacterium tuberculosis* complex transcriptional diversity

Chiner-Oms, Álvaro; González-Candelas, Fernando; Comas, Iñaki (2018)

**Publisher:** Nature Publishing Group

**Languages:** English

**Types:** Article

**Subjects:**

**Identifiers:** doi:10.1038/s41598-018-22237-5

13 Páginas, 7 figuras. Contiene información suplementaria en: 10.1038/s41598-018-22237-5

LINK TO PROJECT LINK TO RESEARCH DATA

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@article{Chiner-Oms, Álvaro, González-Candelas, Fernando, Comas, Iñaki, 2018, title={Gene expression models based on a reference laboratory strain are poor predictors of *Mycobacterium tuberculosis* complex transcriptional diversity}, publisher={Nature Publishing Group}, author=

## 4. Indexación por OpenAire



# CASO 2: Publicación en revista de suscripción y subida de postprint en DIGITAL.CSIC

## 2. Publicación de resultados bajo acceso por suscripción

## 3. Depósito y marcado en DIGITAL CSIC

**CORDIS**  
Community Research and Development Information Service

European Commission > CORDIS > Projects and Results > Pre-Operational Marine Service Continuity in Transition towards Copernicus

**MyOcean FO**  
Project ID: 633085  
Funded under:  
H2020-EU.2.1.6 - INDUSTRIAL LEADERSHIP - Leadership in enabling and industrial technologies - Space

**Pre-Operational Marine Service Continuity in Transition towards Copernicus**  
From 2014-10-01 to 2015-05-31, closed project

**Project details**

<b>Total cost:</b> EUR 6 000 000,04	<b>Topic(s):</b> SPACE - SPACE
<b>EU contribution:</b> EUR 6 000 000	<b>Call for proposal:</b> H2020-Idelic-2014-20
<b>Coordinated in:</b> France	<b>Funding scheme:</b> CSA - Coordination and support action

**Objective**

The main objective of the MyOcean Follow On project will be to operate a rigorous, robust and sustainable Ocean Monitoring and Forecasting component of the pre-operational Copernicus Marine Service delivering ocean physical state and ecosystem information to intermediate and downstream users in the areas of marine safety, marine resources, marine and coastal environment and weather, climate and seasonal forecasting. This is highly consistent with the objective of the HORIZON...

**Report Summaries**

Periodic Reporting for period 1 - MyOcean FO (Pre-Operational Marine Service Continuity in Transition towards Copernicus)

Available online at [www.sciencedirect.com](http://www.sciencedirect.com)

**ScienceDirect**

Advances in Space Research 56 (2015) 596–604

**Improved satellite altimeter mapped sea level anomalies in the Mediterranean Sea: A comparison with tide gauges**

Marta Marcos<sup>a,\*</sup>, Ananda Pascual<sup>a</sup>, Isabelle Pujol<sup>b</sup>

<sup>a</sup>IMEDEA (UIB-CSIC), Esporles, Spain  
<sup>b</sup>CLS, Toulouse, France

Received 27 October 2014; received in revised form 21 April 2015; accepted 22 April 2015  
Available online 29 April 2015

**Abstract**

The new gridded Mediterranean sea level anomaly product recently released by AVISO (DT14) is evaluated and compared with the earlier version (DT10) at which it is aimed to substitute. Differences between the two products are found along coastal regions, where the new version captures more variability (up to 10% more) and trends locally differ by up to 1 mm/yr for the altimetric period. Coastal tide gauge observations have therefore been used as the basis for quantifying changes in DT14. Correlation and variance reduction in available monthly tide gauge time series are improved in more than 80% of the selected sites by up to 0.2 and 5 cm<sup>2</sup>, respectively. This resulted in an overall higher skill to recover coastal low frequency (with periods larger than a few months) sea level signals. Results for higher-order percentiles were also explored and showed different performances depending on the site, although with a slight overall improvement. A comparison with tide gauges on a daily basis using wavelet analysis reveals that altimetry gridded products are not capable of recovering higher frequency (a few days) coastal sea level signals despite some advances have been achieved thanks to the daily temporal sampling of DT14.

**Keywords:** Mediterranean Sea; Sea level; Satellite altimetry; Tide gauges

**1. Introduction**

Since the early nineties, satellite altimetry has become an essential tool in oceanographic research with applications in sea level changes, mesoscale variability or propagating ocean Rossby waves, among others (Cazenave and Llovel, 2010; Le Traon, 2013; Cipolletti et al., 2010; Calafat and Marcos, 2012). During the last 20 years, many efforts have been devoted to data processing and development of geophysical corrections that allowed reaching the current maturity of the sea surface height observations with interpolated products, thus facilitating the investigation of ocean mesoscale variability (Pascual et al., 2000; Pascual et al., 2009). Regional altimetry gridded sea surface height products deserve special attention, as they have been developed using processing adapted to areas of particular oceanographic interest with higher spatial resolution than the global products. This is the case of the Mediterranean Sea, where products are developed with a resolution of 1/8 of degree and that is considered a reduced scale ocean laboratory, where processes can be studied at smaller scales than in other oceanic regions (Internal Rossby Radius is

DIGITAL CSIC > Recursos Educativos > Instituto Mediterraneo de Estudios Avanzados (IMEDEA) > (IMEDEA) Artículos

English español

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**Título:** Improved satellite altimeter mapped sea level anomalies in the Mediterranean Sea: A comparison with tide gauges

**Autor:** Marcos, Marta; Pascual, Ananda; Pujol, Isabelle

**Palabras clave:** Sea level; Satellite altimetry; Mediterranean Sea; Tide gauges

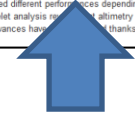
**Fecha de publicación:** 15-ago-2015

**Editor:** Elsevier

**Citación:** Advances in Space Research 56(4): 596-604 (2015)

**Resumen:** The new gridded Mediterranean sea level anomaly product recently released by AVISO (DT14) is evaluated and compared with the earlier version (DT10) at which it is aimed to substitute. Differences between the two products are found along coastal regions, where the new version captures more variability (up to 10% more) and trends locally differ by up to 1 mm/yr for the altimetric period. Coastal tide gauge observations have therefore been used as the basis for quantifying changes in DT14. Correlation and variance reduction in available monthly tide gauge time series are improved in more than 80% of the selected sites by up to 0.2 and 5 cm<sup>2</sup>, respectively. This resulted in an overall higher skill to recover coastal low frequency (with periods larger than a few months) sea level signals. Results for higher-order percentiles were also explored and showed different performances depending on the site, although with a slight overall improvement. A comparison with tide gauges on a daily basis using wavelet analysis reveals that altimetry gridded products are not capable of recovering higher frequency (a few days) coastal sea level signals despite some advances have been achieved thanks to the daily temporal sampling of DT14.

**Versión del editor:** <http://dx.doi.org/10.1016/j.asr.2015.04.027>



## 1. Aprobación de la propuesta

**OpenAIRE**

**Improved satellite altimeter mapped sea level anomalies in the Mediterranean Sea: A comparison with tide gauges**

Marcos, Marta; Pascual, Ananda; Pujol, Isabelle (2015)

**Publisher:** Elsevier

**Languages:** English

**Types:** Article

**Subjects:** Sea level, Satellite altimetry, Mediterranean Sea, Tide gauges

**Identifiers:** doi:10.1016/j.asr.2015.04.027

The new gridded Mediterranean sea level anomaly product recently released by AVISO (DT14) is evaluated and compared with the earlier version (DT10) at which it is aimed to substitute. Differences between the two products are found along coastal regions, where the new version captures more variability (up to 10% more) and trends locally differ by up to 1 mm/yr for the altimetric period. Coastal tide gauge observations have therefore been used as the basis for quantifying changes in DT14. Correlation and variance reduction in available monthly tide gauge time series are improved in more than 80% of the selected sites by up to 0.2 and 5 cm<sup>2</sup>, respectively. This resulted in an overall higher skill to recover coastal low frequency (with periods larger than a few months) sea level signals. Results for higher-order percentiles were also explored and showed different performances depending on the site, although with a slight overall improvement. A comparison with tide gauges on a daily basis using wavelet analysis reveals that altimetry gridded products are not capable of recovering higher frequency (a few days) coastal sea level signals despite some advances have been achieved thanks to the daily temporal sampling of DT14.

**LINK TO PROJECT** **LINK TO RESEARCH DATA**

**References (0)** **Related Research Data (0)** **Similar Publications (1)**

No references.

**Improved satellite altimeter mapped sea level anomalies in the Mediterranean Sea: a comparison with tide gauges**

Marta Marcos<sup>a,1</sup>, Ananda Pascual<sup>a</sup>, Isabelle Pujol<sup>b</sup>

<sup>a</sup>IMEDEA (UIB-CSIC), Esporles, Spain  
<sup>b</sup>CLS, Toulouse, France

*Revised Version*

*Espores, 18 February, 2015*

\* Corresponding author address: Miquel Marqués, 21, 07190, Esporles, Spain,  
[marta.marcos@uib.es](mailto:marta.marcos@uib.es)

## 4. Indexación por OpenAire

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Título:

Formation of the BiAg<sub>2</sub> surface alloy on lattice-mismatched interfaces

Autor:

Abd El-Fattah, Z. M.  Lutz, P.; Piquero-Zulaica, Ignacio; Lobo-Checa, Jorge  Schiller, Frederik  Bentmann, Hendrik; Ortega  Reinert, Friedrich

Fecha de publicación:

2016

Editor:

American Physical Society

Citación:

Physical Review B 94(15): 155447 (2016)

Resumen:

We report on the growth of a monolayer-thick BiAg<sub>2</sub> surface alloy on thin Ag films grown on Pt(111) and Cu(111). Using low energy electron diffraction (LEED), angle resolved photoemission spectroscopy (ARPES), and scanning tunneling microscopy (STM) we show that the surface structure of the 13 ML Bi/x-ML Ag/Pt(111) system (x=2) is strongly affected by the annealing temperature required to form the alloy. As judged from the characteristic (3x3)R30 LEED pattern, the BiAg<sub>2</sub> alloy is partially formed at room temperature. A gentle, gradual increase in the annealing temperatures successively results in the formation of a pure BiAg<sub>2</sub> phase, a combination of that phase with a (2x2) superstructure, and finally the pure (2x2) phase, which persists at higher annealing temperatures. These results complement recent work reporting the (2x2) as a predominant phase, and attributing the absence of BiAg<sub>2</sub> alloy to the strained Ag/Pt interface. Likewise, we show that the growth of the BiAg<sub>2</sub> alloy on similarly lattice-mismatched 1 and 2 ML Ag-Cu(111) interfaces also requires a low annealing temperature, whilst higher temperatures result in BiAg<sub>2</sub> clustering and the formation of a BiCu<sub>2</sub> alloy. The demonstration that the BiAg<sub>2</sub> alloy can be formed on thin Ag films on different substrates presenting a strained interface has the prospect of serving as bases for technologically relevant systems, such as Rashba alloys interfaced with magnetic and semiconductor substrates.

Versión del editor:

<https://doi.org/10.1103/PhysRevB.94.155447>

URI:

<http://hdl.handle.net/10261/148459>

DOI:

10.1103/PhysRevB.94.155447

Identificadores:

doi: 10.1103/PhysRevB.94.155447  
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e-issn: 2469-9969

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Detalles del documento

Formation of the BiAg<sub>2</sub> surface alloy on lattice-mismatched interfaces

Creador(s):

Abd El-Fattah, Z. M.  Lutz, P.  Piquero-Zulaica, Ignacio  Lobo-Checa, Jorge  Schiller, Frederik  Bentmann, Hendrik 

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Inglés

Materia(s):

American Physical Society

Editor(es):

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2017-04-19T07:11:09Z

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MINECO/ICTI2013-2016/MAT2013-46593-C6-4-P, Publisher's version, <https://doi.org/10.1103/PhysRevB.94.155447>, Sí

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1. Depósito y difusión en acceso abierto de un artículo resultado de proyecto Plan Estatal 2013-2016

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- Gruppo Entomologico Toscano - Gruppo Entomologico Toscano - 12-Apr-2018
- MayDay Group - MayDay Group - 11-Apr-2018
- Universidad de Jaén - Universidad de Jaén - 05-Apr-2018

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<a href="#">The Lancet Child &amp; Adolescent Health</a>	2352-4642	6 months
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Subject ?

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Published by:  
The National Academy of Sciences

Main subject area:  
Interdisciplinary Sciences

Peer review type:  
Conventional

ISSN:  
1091-6490

Breadth of subject area:  
All of science

Peer review openness:  
Closed, single blind

Last checked date:  
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Scope:  
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Allows green OA:  
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Length restrictions:  
Strong

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No

Provides altmetrics:  
Altmetric

Has membership system:  
None

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Yes

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0001-4575	<a href="#">Accident Analysis and Prevention</a>	Hybrid	USD	3550.00
0155-9982	<a href="#">Accounting Forum</a>	Hybrid	USD	1100.00
0361-3682	<a href="#">Accounting, Organizations and Society</a>	Hybrid	USD	1800.00
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Wiley-Blackwell	€10,144,840	4337	€2,339	€706	10.57%
Public Library of Science (PLOS)	€8,445,514	6056	€1,395	€395	8.80%
Springer Science + Business Media	€5,479,145	3655	€1,499	€507	5.71%
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BMJ	€2,277,943	1024	€2,225	€682	2.37%
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APC: 25000IDR

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- [Open access policies and requirements in Horizon 2020](#), Jean-François Dechamp, DG RTD A.6, Febrero 2018
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